SEQUENCE LISTING

CDRs For FR1-H7 Amino Acid Sequences

VH (human heavy chain subclass I)
CDR1 **SEQ ID NO:1**   DYYMH
CDR2 **SEQ ID NO:2**   LVDPEDGETIYAEKFQG
CDR3 **SEQ ID NO:3**   DDYMDV

VL (human kappa light chain subgroup III)
CDR1 **SEQ ID NO:4**   RASQSVSGSALA
CDR2 **SEQ ID NO:5**   DASSRAT
CDR3 **SEQ ID NO:6**   QQYGSSPLT

Variable Region of FR1-H7 Heavy Chain

Amino Acid Sequence
SEQ ID NO:7
MAEVQLVQSGAEVKKPGASVKVSCKVSGYTFTDYYMHWVQQAPGKGLEWMGLVDPEDGET
IYAEKFQGRVTITADTSTDTAYMELSSLRSEDTAVYYCARDDYMDVWGKGTLVTVSSAST
KGP

Variable Region of FR1-H7 Light Chain

Amino Acid Sequence
SEQ ID NO:8
LETTLTQSPDTLSLSPGEGATLSCRASQSVSGSALAWYQQKPGQAPRLLIYDASSRATGV
PDRFSGSGSGADFSLTISRLEPEDFAVYSCQQYGSSPLTFGPGTKVDVKRTVAAPSVFIF
PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVD

CDRs For FR1-A1 Amino Acid Sequences

VH (human heavy chain subclass I)
CDR1 **SEQ ID NO:9**   GYYMH
CDR2 **SEQ ID NO:10**   RIIPILGIANYAQKFQG
CDR3 **SEQ ID NO:11**   GGDLGGMDV

VL (human kappa light chain subgroup III)
CDR1 **SEQ ID NO:12**   RSSQSLRHSNGYNYLD
CDR2 **SEQ ID NO:13**   LASNRAS
CDR3 **SEQ ID NO:14**   MQALQIPPT

Variable Region of FR1-A1 Heavy Chain

Amino Acid Sequences
SEQ ID NO:15.
MAQVQLVQSGAEVKKPGSSVKVSCKASGQTFTGYYMHWVRQAPGQGLEWMGRIIPILGIA
NYAQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCARGGDLGGMDVWGQG

Variable Region of FR1-A1 Light Chain

Amino Acid Sequences
SEQ ID NO:16
LEIVLTQSPLSLPVTPGEPASISCRSSQSLRHSNGYNYLDWYLQKPGQSPQLLIYLASNR
ASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQIPPTFGPGTKVDIKRTVAA

CDRs For FR1-4H Amino Acid Sequences

Variable Heavy Chain
CDR1 **SEQ ID NO:17**   SYYWS
CDR2 **SEQ ID NO:18**   YIYYSGSTNYNPSLKS
CDR3 **SEQ ID NO:19**   EYYYDSSGYYFYAFDI

Variable Light Chain]
CDR1 **SEQ ID NO:20**   SGSSSNIGSNYVY
CDR2 **SEQ ID NO:21**   RNNQRPS
CDR3 **SEQ ID NO:22**   AAWDDSLSGWV

Variable Region Heavy Chain FR1-4H

Amino Acid Sequences
SEQ ID NO:23
QVQLVEFGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGY   50
IYYSGSTNYNPSLKSRVAISVDTSKNQFSLKLSSVTAADTAVYYCAREYY   100
YDSSGYYFYAFDIWGQGTTVTVSS   124

Variable Region Light Chain

Amino Acid Sequence
SEQ ID NO:24
LPVLTQPPSASGTPGQRVSISCSGSSSNIGSNYVYWYQQLPGTAPKLLIF   50
RNNQRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYCAAWDDSLSGWV   100
FGGGTKLTVLG   111

CDRs For FR1-H7 Nucleic Acid Sequences

VH (human heavy chain subclass I)
CDR1 **SEQ ID NO:25**   GACTACTACATGCAC
CDR2 **SEQ ID NO:26**   CTTGTTGATCCTGAAGATGGTGAAACAATCTACGCAGA
GAAGTTCCAGGGC
CDR3 **SEQ ID NO:27**   GATGACTACATGGACGTC

VL (human kappa light chain subgroup III)
CDR1 **SEQ ID NO:28**   AGGGCCAGTCAGAGTGTTAGCGGCAGTGCGTTGGCC
CDR2 **SEQ ID NO:29**   GATGCATCCAGTAGGGCCACT
CDR3 **SEQ ID NO:30**   CAGCAATATGGTAGCTCACCTCTCACT

Variable Region of FR1-H7 Heavy Chain DNA Sequence
SEQ ID NO:31

ATGGCCGAGGTGCAGCTGGTGCAGTCTGGGGGCTGAGGTGAAGAAGCCTGGGGGCCTCAGTG
AAGGTTTCCTGCAAGGTTTCTGGATACACCTTCACCGACTACTACATGCACTGGGTGCAA
CAGGCCCCTGGAAAAGGGCTTGAGTGGATGGGACTTGTTGATCCTGAAGATGGTGAAACA
ATCTACGCAGAGAAGTTCCAGGGCAGAGTCACCATAACCGCGGACACGTCTACAGACACA
GCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGA
GATGACTACATGGACGTCTGGGGCAAAGGCACCCTGGTCACCGTCTCAAGCGCCTCCACC
AAGGGCCCA

Variable Region of FR1-H7 Light Chain DNA Sequence
SEQ ID NO:32
CTTGAAACGACACTCACGCAGTCTCCAGACACCCTGTCTTTGTCTCCAGGAGAAGGAGCC
ACCCTCTCCTGTAGGGCCAGTCAGAGTGTTAGCGGCAGTGCGTTGGCCTGGTACCAGCAG
AAACCTGGCCAGGCTCCCAGACTCCTCATCTATGATGCATCCAGTAGGGCCACTGGCGTC
CCAGACAGGTTCAGTGGCAGTGGGTCTGGGCAGACTTCAGTCTCACCATCAGCAGACTG
GAGCCTGAAGATTTTGCAGTGTATTCCTGTCAGCAATATGGTAGCTCACCTCTCACTTTC
GGCCCTGGGACCAAAGTGGATGTCAAACGAACTGTGGCTGCACCATCTGTCTTCATCTTC
CCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAAC
TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATT

CDRs For FR1-A1 Nucleic Acid Sequences

VH (human heavy chain subclass I)
CDR1 **SEQ ID NO:33**   GGCTACTATATGCAC
CDR2 **SEQ ID NO:34**   AGGATCATCCCTATCCTTGGTATAGCAAAC
TACGCACAGAAGTTCCAGGGC
CDR3 **SEQ ID NO:35**   GGAGGAGATCTGGGCGGTATGGACGTC

VL (human kappa light chain subgroup III)
CDR1 **SEQ ID NO:36**   AGGTCTAGTCAGAGCCTCCGGCATAGTAAT
GGATACAACTATTTGGAT
CDR2 **SEQ ID NO:37**   TTGGCTTCTAATCGGGCCTCC
CDR3 **SEQ ID NO:38**   ATGCAAGCTCTACAAATTCCTCCGACT

Variable Region of FR1-A1 Heavy Chain

DNA Sequence
SEQ ID NO:39
ATGGCCCAGGTCCAGCTGGTGCAGTCTGGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTG
AAGGTCTCCTGCAAGGCTTCTGGATCGACCTTCACCGGCTACTATATGCACTGGGTGCGA
CAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCCTTGGTATAGCA
AACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACA
GCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTACTACTGTGCGAGA
GGAGGAGATCTGGGCGGTATGGACGTCTGGGGCCAAGGGA

Variable Region of FR1-A1 Light Chain

DNA Sequences
SEQ ID NO:40

CTTGAAATTGTGCTGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCC
TCCATCTCCTGCAGGTCTAGTCAGAGCCTCCGGCATAGTAATGGATACAACTATTTGGAT
TGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGGCTTCTAATCGG
GCCTCCGGGGTCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAA
ATCAGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAAGCTCTACAAATT
CCTCCGACTTTCGGCCCTGGGACCAAAGTGGATATCAAACGAACTGTGGCTGCA

CDRs For FR1-4H Nucleic Acid Sequences

Variable Heavy Chain
CDR1 **SEQ ID NO:41**   AGTTACTACTGGAGC
CDR2 **SEQ ID NO:42**
     TATATCTATTACAGTGGGAGCACCAACTACAACCCCTCCCTCAAGAGT
CDR3 **SEQ ID NO:43**
     GAGTATTACTATGATAGTAGTGGTTATTACTTTTATGCTTTTGATATC

Variable Light Chain]
CDR1 **SEQ ID NO:44**   TCTGGAAGCAGCTCCAACATCGGAAGTAATTATGTATAC
CDR2 **SEQ ID NO:45**   AGGAATAATCAGCGGCCCTCA
CDR3 **SEQ ID NO:46**   GCAGCATGGGATGACAGCCTGAGTGGTTGGGTG

Variable Region Heavy Chain FR1-4H

DNA Sequences
SEQ ID NO:47

CAGGTGCAGCTGGTGGAGTTTGGCCCAGGACTGGTGAAGCCTTCGGAGAC	50
CCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGTAGTTACTACT	100
GGAGCTGGATCCGGCAGCCCCCAGGGAAGGGACTGGAGTGGATTGGGTAT	150
ATCTATTACAGTGGGAGCACCAACTACAACCCCTCCCTCAAGAGTCGAGT	200
CGCCATATCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCT	250
CTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCGAGAGAGTATTAC	300
TATGATAGTAGTGGTTATTACTTTTATGCTTTTGATATCTGGGGCCAAGG	350
GACCACGGTCACCGTCTCAAGC	372

Variable Region Light Chain

DNA Sequence
SEQ ID NO:48

CTGCCTGTGCTGACTCAGCCCCCCTCAGCGTCTGGGACCCCCGGGCAGAG	50
GGTCTCCATCTCTTGTTCTGGAAGCAGCTCCAACATCGGAAGTAATTATG	100
TATACTGGTACCAGCAGCTCCCAGGAACGGCCCCCAAACTCCTCATCTTT	150
AGGAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA	200
GTCTGGCACTTCAGCCTCCCTGGCCATCAGTGGGCTCCGGTCCGAGGATG	250
AGGCTGATTATTACTGTGCAGCATGGGATGACAGCCTGAGTGGTTGGGTG	300
TTCGGCGGAGGGACCAAGCTGACCGTCCTAGGT	333